

## SEQUENCE LISTING



<110> Smith, Richard  
Dodd, Ian  
Mossakowska, Danuta, Ewa, Irena

<120> CONJUGATES OF SOLUBLE PEPTIDIC COMPOUNDS WITH  
MEMBRANE-BINDING AGENTS

<130> 088362/0112

<140> 09/214,913

<141> 1999-03-16

<150> 2260288

<151> 1997-07-08

<150> 9614871.3

<151> 1996-07-15

<160> 51

<170> PatentIn Ver. 2.1

<210> 1

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
Oligonucleotide used to anneal to oligonucleotide  
of SEQ ID NO.2

<400> 1

gcaccgcagt gcatcatccc gaacaaatgc taataaa

37

<210> 2

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
Oligonucleotide used to anneal to oligonucleotide  
of SEQ ID NO.1

<400> 2

agcttttatt agcatttggt cgggatgatg cactgcg

37

<210> 3

<211> 85

<212> DNA

<213> Artificial Sequence

of SEQ ID NO.4 to generate fragment 4

```
<400> 3
gcaccgcagt gcatcatccc gaacaaagac ggtccgaaaa agaagaaaaa gaaatctccg 60
tccaaatctt ccggttgcta ataaa                                     85
```

```
<210> 4
<211> 85
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> Description of Artificial Sequence:
      Oligonucleotide used to anneal to oligonucleotide
      of SEQ ID NO.3 to generate fragment 4
```

```
<400> 4
agcttttatt agcaaccgga agatttgac ggagatttct tttcttctt tttcggaccg 60
tctttgttcg ggatgatgca ctgcg                                     85
```

```
<210> 5
<211> 17
<212> PRT
<213> Artificial Sequence
```

```
<220>
<221> UNSURE
<222> (17)
<223> NH2 group is linked to the C-terminal cysteine
```

```
<220>
<223> Description of Artificial Sequence: Peptide used
      to synthesie MSWP-1
```

```
<400> 5
Gly Ser Ser Lys Ser Pro Ser Lys Lys Lys Lys Lys Lys Pro Gly Asp
  1             5             10             15
```

Cys

```
<210> 6
<211> 198
<212> PRT
<213> Artificial Sequence
```

```
<220>
<223> Description of Artificial Sequence: The petide
      sequence correpsonds to short consensus repeats
      1-3 of CR1 with a C-terminal cysteine
```

```
<400> 6
Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
  1             5             10             15
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Arg | Pro | Gly | Tyr | Ser | Gly | Arg | Pro | Phe | Ser | Ile | Ile | Cys | Leu | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Ser | Val | Trp | Thr | Gly | Ala | Lys | Asp | Arg | Cys | Arg | Arg | Lys | Ser | Cys |
|     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Arg | Asn | Pro | Pro | Asp | Pro | Val | Asn | Gly | Met | Val | His | Val | Ile | Lys | Gly |
|     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |
| Ile | Gln | Phe | Gly | Ser | Gln | Ile | Lys | Tyr | Ser | Cys | Thr | Lys | Gly | Tyr | Arg |
|     |     |     |     | 85  |     |     |     |     |     |     | 90  |     |     |     |     |
| Leu | Ile | Gly | Ser | Ser | Ser | Ala | Thr | Cys | Ile | Ile | Ser | Gly | Asp | Thr | Val |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 110 |     |
| Ile | Trp | Asp | Asn | Glu | Thr | Pro | Ile | Cys | Asp | Arg | Ile | Pro | Cys | Gly | Leu |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 125 |     |
| Pro | Pro | Thr | Ile | Thr | Asn | Gly | Asp | Phe | Ile | Ser | Thr | Asn | Arg | Glu | Asn |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 140 |     |
| Phe | His | Tyr | Gly | Ser | Val | Val | Thr | Tyr | Arg | Cys | Asn | Pro | Gly | Ser | Gly |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 155 | 160 |
| Gly | Arg | Lys | Val | Phe | Glu | Leu | Val | Gly | Glu | Pro | Ser | Ile | Tyr | Cys | Thr |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Ser | Asn | Asp | Asp | Gln | Val | Gly | Ile | Trp | Ser | Gly | Pro | Ala | Pro | Gln | Cys |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Ile | Ile | Pro | Asn | Lys | Cys |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

```
<210> 7
<211> 214
<212> PRT
<213> Artificial Sequence
```

```
<220>
<223> Description of Artificial Sequence: Short
consensus repeats 1-3 of CR1 with an additional 17
C-terminal amino acids
```

```

<400> 7
Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
  1             5             10             15
Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
          20             25             30
Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
          35             40             45

```

Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly  
 65 70 75 80  
 Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg  
 85 90 95  
 Leu Ile Gly Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val  
 100 105 110  
 Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu  
 115 120 125  
 Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn  
 130 135 140  
 Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly  
 145 150 155 160  
 Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr  
 165 170 175  
 Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys  
 180 185 190  
 Ile Ile Pro Asn Lys Asp Gly Pro Lys Lys Lys Lys Lys Lys Ser Pro  
 195 200 205  
 Ser Lys Ser Ser Gly Cys  
 210

<210> 8  
 <211> 215  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <221> UNSURE  
 <222> (198)..(199)  
 <223> Residues 1-198 are a first polypeptide chain and  
 residues 199-215 are a second polypeptide chain  
 linked by a disulphide bond formed between the  
 cysteines at positions 198 and 199

<220>  
 <221> UNSURE  
 <222> (215)  
 <223> The C-terminal glycine is linked to an  
 N-(Myristoyl) group

<220>  
 <221> UNSURE  
 <222> (198)  
 <223> The cysteine at position 198 is -Cys-COOH

<223> The cysteine at position 199 is CONH2-Cys-

 $\langle 220 \rangle$ 

<223> Description of Artificial Sequence:

[SCR1-3] - Cys-S-S- [MSWP-1]

<400> 8

Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn

Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu  
20 25 30

Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys  
35 40 45

Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys  
50 55 60

Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly  
65 70 75 80

Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg  
85 90 95

Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val  
100 105 110

Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu  
115 120 125

Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn  
130 135 140

Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly  
145 150 155 160

Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr  
165 170 175

Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys  
180 185 190

Ile Ile Pro Asn Lys Cys Cys Asp Gly Pro Lys Lys Lys Lys Lys Lys  
195 200 205

Ser Pro Ser Lys Ser Ser Gly  
210 215

<210> 9

 $\langle 211 \rangle$  231

&lt;212&gt; PRT

<213> Artificial Sequence

<223> Residues 1-214 are a first polypeptide chain and residues 215-231 are a second polypeptide chain linked by a disulphide bond formed between the cysteines at positions 214 and 215

<220>

<221> UNSURE

<222> (231)

<223> The C-terminal glycine is linked to an N-[Myristoyl] group

<220>

<223> Description of Artificial Sequence: [SCR1-3/switch fusion] disulphide linked to [MSWP-1]

<220>

<221> UNSURE

<222> (214)

<223> The cysteine at position 214 is -Cys-COOH

<220>

<221> UNSURE

<222> (215)

<223> The cysteine at position 215 is CONH2-Cys-

<400> 9

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Cys | Asn | Ala | Pro | Glu | Trp | Leu | Pro | Phe | Ala | Arg | Pro | Thr | Asn |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Thr | Asp | Glu | Phe | Glu | Phe | Pro | Ile | Gly | Thr | Tyr | Leu | Asn | Tyr | Glu |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Arg | Pro | Gly | Tyr | Ser | Gly | Arg | Pro | Phe | Ser | Ile | Ile | Cys | Leu | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Ser | Val | Trp | Thr | Gly | Ala | Lys | Asp | Arg | Cys | Arg | Arg | Lys | Ser | Cys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Asn | Pro | Pro | Asp | Pro | Val | Asn | Gly | Met | Val | His | Val | Ile | Lys | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Gln | Phe | Gly | Ser | Gln | Ile | Lys | Tyr | Ser | Cys | Thr | Lys | Gly | Tyr | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ile | Gly | Ser | Ser | Ser | Ala | Thr | Cys | Ile | Ile | Ser | Gly | Asp | Thr | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Trp | Asp | Asn | Glu | Thr | Pro | Ile | Cys | Asp | Arg | Ile | Pro | Cys | Gly | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Pro | Thr | Ile | Thr | Asn | Gly | Asp | Phe | Ile | Ser | Thr | Asn | Arg | Glu | Asn |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | His | Tyr | Gly | Ser | Val | Val | Thr | Tyr | Arg | Cys | Asn | Pro | Gly | Ser | Gly |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys  
 180 185 190

Ile Ile Pro Asn Lys Asp Gly Pro Lys Lys Lys Lys Lys Lys Ser Pro  
 195 200 205

Ser Lys Ser Ser Gly Cys Cys Asp Gly Pro Lys Lys Lys Lys Lys Lys  
 210 215 220

Ser Pro Ser Lys Ser Ser Gly  
 225 230

<210> 10  
 <211> 1947  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <221> UNSURE  
 <222> (1930)..(1931)  
 <223> Residues 1-1930 are a first polypeptide chain and  
 residues 1931-1947 are a second polypeptide chain  
 linked by a disulphide bond formed between the  
 cysteines at positions 1930 and 1931

<220>  
 <221> UNSURE  
 <222> (1947)  
 <223> The C-terminal glycine is linked to an  
 N-[Myristoyl] group

<220>  
 <223> Description of Artificial Sequence: [CR1: 1-1929]  
 - Cys-S-S-[MSWP-1]

<220>  
 <221> UNSURE  
 <222> (1930)  
 <223> The cysteine at position 1930 is -Cys-COOH

<220>  
 <221> UNSURE  
 <222> (1931)  
 <223> The Cysteine at position 1931 is CONH2-Cys-

<400> 10  
 Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu  
 1 5 10 15

Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys  
 20 25 30

Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn

Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg  
 50 55 60  
 Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile  
 65 70 75 80  
 Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu  
 85 90 95  
 Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile  
 100 105 110  
 Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro  
 115 120 125  
 Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe  
 130 135 140  
 His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly  
 145 150 155 160  
 Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser  
 165 170 175  
 Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile  
 180 185 190  
 Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val  
 195 200 205  
 Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg  
 210 215 220  
 Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln  
 225 230 235 240  
 Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys  
 245 250 255  
 Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys  
 260 265 270  
 Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly  
 275 280 285  
 Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp  
 290 295 300  
 Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe  
 305 310 315 320  
 Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln  
 325 330 335  
 Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys



Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp  
 355 360 365  
 Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro  
 370 375 380  
 Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro  
 385 390 395 400  
 Phe Gly Lys Ala Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly  
 405 410 415  
 Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp  
 420 425 430  
 Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile  
 435 440 445  
 Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys  
 450 455 460  
 Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr  
 465 470 475 480  
 Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu  
 485 490 495  
 Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser  
 500 505 510  
 Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Thr  
 515 520 525  
 Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His  
 530 535 540  
 Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala  
 545 550 555 560  
 Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly  
 565 570 575  
 Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu  
 580 585 590  
 Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser  
 595 600 605  
 Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys  
 610 615 620  
 Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln  
 625 630 635 640  
 Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile  
 645 650 655

Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu  
 660 665 670  
 Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys  
 675 680 685  
 Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg  
 690 695 700  
 Val Cys Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg  
 705 710 715 720  
 Asp Lys Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu  
 725 730 735  
 Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln  
 740 745 750  
 Gly Asp Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp  
 755 760 765  
 Asp Phe Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn  
 770 775 780  
 Leu Gln Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln  
 785 790 795 800  
 Leu Lys Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser  
 805 810 815  
 Leu Trp Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser  
 820 825 830  
 Pro Pro Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val  
 835 840 845  
 Phe Pro Phe Gly Lys Ala Val Asn Tyr Thr Cys Asp Pro His Pro Asp  
 850 855 860  
 Arg Gly Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr  
 865 870 875 880  
 Ser Asp Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys  
 885 890 895  
 Gly Ile Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys  
 900 905 910  
 Leu Lys Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu  
 915 920 925  
 Lys Tyr Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr  
 930 935 940  
 Cys Leu Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg  
 945 950 955

Lys Ser Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val His Val  
 965 970 975  
 Ile Thr Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr  
 980 985 990  
 Gly His Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly  
 995 1000 1005  
 Asn Thr Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro  
 1010 1015 1020  
 Cys Gly Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn  
 1025 1030 1035 1040  
 Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Leu  
 1045 1050 1055  
 Gly Ser Arg Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile  
 1060 1065 1070  
 Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala  
 1075 1080 1085  
 Pro Gln Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn  
 1090 1095 1100  
 Gly Ile Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val  
 1105 1110 1115 1120  
 Val Glu Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg  
 1125 1130 1135  
 Val Lys Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys  
 1140 1145 1150  
 Ser Arg Val Cys Gln Pro Pro Pro Glu Ile Leu His Gly Glu His Thr  
 1155 1160 1165  
 Pro Ser His Gln Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser  
 1170 1175 1180  
 Cys Glu Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Leu His Cys Thr  
 1185 1190 1195 1200  
 Pro Gln Gly Asp Trp Ser Pro Glu Ala Pro Arg Cys Ala Val Lys Ser  
 1205 1210 1215  
 Cys Asp Asp Phe Leu Gly Gln Leu Pro His Gly Arg Val Leu Phe Pro  
 1220 1225 1230  
 Leu Asn Leu Gln Leu Gly Ala Lys Val Ser Phe Val Cys Asp Glu Gly  
 1235 1240 1245  
 Phe Arg Leu Lys Gly Ser Ser Val Ser His Cys Val Leu Val Gly Met

Arg Ser Leu Trp Asn Asn Ser Val Pro Val Cys Glu His Ile Phe Cys  
 1265 1270 1275 1280  
 Pro Asn Pro Pro Ala Ile Leu Asn Gly Arg His Thr Gly Thr Pro Ser  
 1285 1290 1295  
 Gly Asp Ile Pro Tyr Gly Lys Glu Ile Ser Tyr Thr Cys Asp Pro His  
 1300 1305 1310  
 Pro Asp Arg Gly Met Thr Phe Asn Leu Ile Gly Glu Ser Thr Ile Arg  
 1315 1320 1325  
 Cys Thr Ser Asp Pro His Gly Asn Gly Val Trp Ser Ser Pro Ala Pro  
 1330 1335 1340  
 Arg Cys Glu Leu Ser Val Arg Ala Gly His Cys Lys Thr Pro Glu Gln  
 1345 1350 1355 1360  
 Phe Pro Phe Ala Ser Pro Thr Ile Pro Ile Asn Asp Phe Glu Phe Pro  
 1365 1370 1375  
 Val Gly Thr Ser Leu Asn Tyr Glu Cys Arg Pro Gly Tyr Phe Gly Lys  
 1380 1385 1390  
 Met Phe Ser Ile Ser Cys Leu Glu Asn Leu Val Trp Ser Ser Val Glu  
 1395 1400 1405  
 Asp Asn Cys Arg Arg Lys Ser Cys Gly Pro Pro Pro Glu Pro Phe Asn  
 1410 1415 1420  
 Gly Met Val His Ile Asn Thr Asp Thr Gln Phe Gly Ser Thr Val Asn  
 1425 1430 1435 1440  
 Tyr Ser Cys Asn Glu Gly Phe Arg Leu Ile Gly Ser Pro Ser Thr Thr  
 1445 1450 1455  
 Cys Leu Val Ser Gly Asn Asn Val Thr Trp Asp Lys Lys Ala Pro Ile  
 1460 1465 1470  
 Cys Glu Ile Ile Ser Cys Glu Pro Pro Pro Thr Ile Ser Asn Gly Asp  
 1475 1480 1485  
 Phe Tyr Ser Asn Asn Arg Thr Ser Phe His Asn Gly Thr Val Val Thr  
 1490 1495 1500  
 Tyr Gln Cys His Thr Gly Pro Asp Gly Glu Gln Leu Phe Glu Leu Val  
 1505 1510 1515 1520  
 Gly Glu Arg Ser Ile Tyr Cys Thr Ser Lys Asp Asp Gln Val Gly Val  
 1525 1530 1535  
 Trp Ser Ser Pro Pro Pro Arg Cys Ile Ser Thr Asn Lys Cys Thr Ala  
 1540 1545 1550  
 Pro Glu Val Glu Asn Ala Ile Arg Val Pro Gly Asn Arg Ser Phe Phe

Ser Leu Thr Glu Ile Ile Arg Phe Arg Cys Gln Pro Gly Phe Val Met  
 1570 1575 1580

Val Gly Ser His Thr Val Gln Cys Gln Thr Asn Gly Arg Trp Gly Pro  
 1585 1590 1595 1600

Lys Leu Pro His Cys Ser Arg Val Cys Gln Pro Pro Pro Glu Ile Leu  
 1605 1610 1615

His Gly Glu His Thr Leu Ser His Gln Asp Asn Phe Ser Pro Gly Gln  
 1620 1625 1630

Glu Val Phe Tyr Ser Cys Glu Pro Ser Tyr Asp Leu Arg Gly Ala Ala  
 1635 1640 1645

Ser Leu His Cys Thr Pro Gln Gly Asp Trp Ser Pro Glu Ala Pro Arg  
 1650 1655 1660

Cys Thr Val Lys Ser Cys Asp Asp Phe Leu Gly Gln Leu Pro His Gly  
 1665 1670 1675 1680

Arg Val Leu Leu Pro Leu Asn Leu Gln Leu Gly Ala Lys Val Ser Phe  
 1685 1690 1695

Val Cys Asp Glu Gly Phe Arg Leu Lys Gly Arg Ser Ala Ser His Cys  
 1700 1705 1710

Val Leu Ala Gly Met Lys Ala Leu Trp Asn Ser Ser Val Pro Val Cys  
 1715 1720 1725

Glu Gln Ile Phe Cys Pro Asn Pro Pro Ala Ile Leu Asn Gly Arg His  
 1730 1735 1740

Thr Gly Thr Pro Phe Gly Asp Ile Pro Tyr Gly Lys Glu Ile Ser Tyr  
 1745 1750 1755 1760

Ala Cys Asp Thr His Pro Asp Arg Gly Met Thr Phe Asn Leu Ile Gly  
 1765 1770 1775

Glu Ser Ser Ile Arg Cys Thr Ser Asp Pro Gln Gly Asn Gly Val Trp  
 1780 1785 1790

Ser Ser Pro Ala Pro Arg Cys Glu Leu Ser Val Pro Ala Ala Cys Pro  
 1795 1800 1805

His Pro Pro Lys Ile Gln Asn Gly His Tyr Ile Gly Gly His Val Ser  
 1810 1815 1820

Leu Tyr Leu Pro Gly Met Thr Ile Ser Tyr Thr Cys Asp Pro Gly Tyr  
 1825 1830 1835 1840

Leu Leu Val Gly Lys Gly Phe Ile Phe Cys Thr Asp Gln Gly Ile Trp  
 1845 1850 1855

Ser Gln Leu Asp His Tyr Cys Lys Glu Val Asn Cys Ser Phe Pro Leu

Phe Met Asn Gly Ile Ser Lys Glu Leu Glu Met Lys Lys Val Tyr His  
 1875 1880 1885

Tyr Gly Asp Tyr Val Thr Leu Lys Cys Glu Asp Gly Tyr Thr Leu Glu  
 1890 1895 1900

Gly Ser Pro Trp Ser Gln Cys Gln Ala Asp Asp Arg Trp Asp Pro Pro  
 1905 1910 1915 1920

Leu Ala Lys Cys Thr Ser Arg Ala His Cys Cys Asp Gly Pro Lys Lys  
 1925 1930 1935

Lys Lys Lys Lys Ser Pro Ser Lys Ser Ser Gly  
 1940 1945

<210> 11  
 <211> 215  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <221> UNSURE  
 <222> (198)..(199)  
 <223> Residues 1-198 are a first polypeptide chain and  
 residues 199-215 are a second polypeptide chain  
 linked by a disulphide bond formed between the  
 cysteines at positions 198 and 199

<220>  
 <221> UNSURE  
 <222> (199)  
 <223> The cysteine at position 199 is linked to a  
 NHCOCH3 group

<220>  
 <221> UNSURE  
 <222> (215)  
 <223> The C-terminal lysine is is linked to an  
 N-[Myristoyl]-NH2 group

<220>  
 <223> Description of Artificial Sequence:  
 [SCR1-3]-Cys-S-S-[MSWP-2]

<400> 11  
 Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn  
 1 5 10 15

Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu  
 20 25 30

Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys  
 35 40 45

```

Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly
65              70              75              80

Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg
85              90              95

Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val
100            105            110

Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu
115            120            125

Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn
130            135            140

Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly
145            150            155            160

Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr
165            170            175

Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys
180            185            190

Ile Ile Pro Asn Lys Cys Cys Asp Gly Pro Lys Lys Lys Lys Lys Lys
195            200            205

Ser Pro Ser Lys Ser Ser Lys
210            215

```

```

<210> 12
<211> 213
<212> PRT
<213> Artificial Sequence

```

```

<220>
<221> UNSURE
<222> (198)..(199)
<223> Residues 1-198 are a first polypeptide chain and
      residues 199-213 are a second polypeptide chain
      linked by a disulphide bond formed between the
      cysteines at positions 198 and 199

```

```

<220>
<221> UNSURE
<222> (199)
<223> The cysteine at position 199 is linked to a CONH2
      group

```

```

<220>
<221> UNSURE
<222> (213)
<223> The C-terminal serine is linked to an
      NH-[Myristoyl] group

```

[SCR1-3]-Cys-S-S-[MSWP-3]

&lt;400&gt; 12

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Cys | Asn | Ala | Pro | Glu | Trp | Leu | Pro | Phe | Ala | Arg | Pro | Thr | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Thr | Asp | Glu | Phe | Glu | Phe | Pro | Ile | Gly | Thr | Tyr | Leu | Asn | Tyr | Glu |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Arg | Pro | Gly | Tyr | Ser | Gly | Arg | Pro | Phe | Ser | Ile | Ile | Cys | Leu | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Ser | Val | Trp | Thr | Gly | Ala | Lys | Asp | Arg | Cys | Arg | Arg | Lys | Ser | Cys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Asn | Pro | Pro | Asp | Pro | Val | Asn | Gly | Met | Val | His | Val | Ile | Lys | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Gln | Phe | Gly | Ser | Gln | Ile | Lys | Tyr | Ser | Cys | Thr | Lys | Gly | Tyr | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ile | Gly | Ser | Ser | Ser | Ala | Thr | Cys | Ile | Ile | Ser | Gly | Asp | Thr | Val |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Trp | Asp | Asn | Glu | Thr | Pro | Ile | Cys | Asp | Arg | Ile | Pro | Cys | Gly | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Pro | Thr | Ile | Thr | Asn | Gly | Asp | Phe | Ile | Ser | Thr | Asn | Arg | Glu | Asn |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | His | Tyr | Gly | Ser | Val | Val | Thr | Tyr | Arg | Cys | Asn | Pro | Gly | Ser | Gly |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Arg | Lys | Val | Phe | Glu | Leu | Val | Gly | Glu | Pro | Ser | Ile | Tyr | Cys | Thr |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Asn | Asp | Asp | Gln | Val | Gly | Ile | Trp | Ser | Gly | Pro | Ala | Pro | Gln | Cys |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Ile | Pro | Asn | Lys | Cys | Cys | Lys | Thr | Lys | Ser | Lys | Lys | Lys | Lys | Lys |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |

|     |     |     |     |     |
|-----|-----|-----|-----|-----|
| Lys | Gly | Asp | Lys | Ser |
|     | 210 |     |     |     |

&lt;210&gt; 13

&lt;211&gt; 214

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (198)..(199)

&lt;223&gt; Residues 1-198 are a first polypeptide chain and



<220>

<221> UNSURE

<222> (199)

<223> The cysteine at position 199 is linked to an  
NHCOCH<sub>3</sub> group

<220>

<221> UNSURE

<222> (214)

<223> The C-terminal valine is linked to an -NH(CH<sub>2</sub>)<sub>9</sub>CH<sub>3</sub>  
group.

<220>

<223> Description of Artificial Sequence:

[SCR1-3]-Cys-S-S-[TCPT-1]

<400> 13

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Cys | Asn | Ala | Pro | Glu | Trp | Leu | Pro | Phe | Ala | Arg | Pro | Thr | Asn |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Thr | Asp | Glu | Phe | Glu | Phe | Pro | Ile | Gly | Thr | Tyr | Leu | Asn | Tyr | Glu |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Arg | Pro | Gly | Tyr | Ser | Gly | Arg | Pro | Phe | Ser | Ile | Ile | Cys | Leu | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Ser | Val | Trp | Thr | Gly | Ala | Lys | Asp | Arg | Cys | Arg | Arg | Lys | Ser | Cys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Asn | Pro | Pro | Asp | Pro | Val | Asn | Gly | Met | Val | His | Val | Ile | Lys | Gly |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Gln | Phe | Gly | Ser | Gln | Ile | Lys | Tyr | Ser | Cys | Thr | Lys | Gly | Tyr | Arg |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ile | Gly | Ser | Ser | Ser | Ala | Thr | Cys | Ile | Ile | Ser | Gly | Asp | Thr | Val |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Trp | Asp | Asn | Glu | Thr | Pro | Ile | Cys | Asp | Arg | Ile | Pro | Cys | Gly | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Pro | Thr | Ile | Thr | Asn | Gly | Asp | Phe | Ile | Ser | Thr | Asn | Arg | Glu | Asn |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | His | Tyr | Gly | Ser | Val | Val | Thr | Tyr | Arg | Cys | Asn | Pro | Gly | Ser | Gly |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Arg | Lys | Val | Phe | Glu | Leu | Val | Gly | Glu | Pro | Ser | Ile | Tyr | Cys | Thr |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Asn | Asp | Asp | Gln | Val | Gly | Ile | Trp | Ser | Gly | Pro | Ala | Pro | Gln | Cys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Ile | Pro | Asn | Lys | Cys | Cys | Ser | Ala | Ala | Pro | Ser | Ser | Gly | Phe | Arg |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

Ile Leu Leu Leu Lys Val  
210

<210> 14  
<211> 209  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: SCR1-3 with  
the C-terminal amino acids N195 and K196 replaced  
by a 14 amino acid peptide.

<400> 14  
Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn  
1 5 10 15  
Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu  
20 25 30  
Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys  
35 40 45  
Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys  
50 55 60  
Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly  
65 70 75 80  
Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg  
85 90 95  
Leu Ile Gly Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val  
100 105 110  
Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu  
115 120 125  
Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn  
130 135 140  
Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly  
145 150 155 160  
Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr  
165 170 175  
Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys  
180 185 190  
Ile Ile Pro Thr Asn Ala Asn Lys Ser Leu Ser Ser Ile Ser Cys Gln  
195 200 205  
Thr

<210> 15  
 <211> 53  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:  
     Oligonucleotide used to generate a novel  
     restriction site and a C-terminal cysteine in  
     plasmid pBC04-29  
  
 <400> 15  
 ctggagcggg ccgcacgc agtgcacat cccgaacaaa tgctaataaa agc 53  
  
 <210> 16  
 <211> 53  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:  
     Oligonucleotide used to generate a novel  
     restriction site and C terminal cysteine residue  
     in plasmid pBC04-29  
  
 <400> 16  
 gcttttatta gcatttggtc gggatgatgc actgcggtgc gggcccgctc cag 53  
  
 <210> 17  
 <211> 224  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <221> UNSURE  
 <222> (1)..(209)  
 <223> Positions 1-209 are a first polypeptide chain  
     which is linked to a second polypeptide chain  
     (positions 210-224) by a disulphide linkage  
     between the cysteines at positions 207 and 210.  
  
 <220>  
 <221> UNSURE  
 <222> (210)  
 <223> The cysteine at position 210 is linked to a -CONH2  
     group  
  
 <220>  
 <221> UNSURE  
 <222> (224)  
 <223> The glycine at position 224 is linked to an  
     -NH-[Myristoyl] group  
  
 <220>  
 <223> Description of Artificial Sequence:  
     [SCP1-3/delN195 K196]LTWAKSLSSSSG

&lt;400&gt; 17

Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn  
 1 5 10 15

Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu  
 20 25 30

Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys  
 35 40 45

Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys  
 50 55 60

Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly  
 65 70 75 80

Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg  
 85 90 95

Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val  
 100 105 110

Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu  
 115 120 125

Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn  
 130 135 140

Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly  
 145 150 155 160

Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr  
 165 170 175

Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys  
 180 185 190

Ile Ile Pro Thr Asn Ala Asn Lys Ser Leu Ser Ser Ile Ser Cys Gln  
 195 200 205

Thr Cys Asp Gly Pro Lys Lys Lys Lys Lys Ser Lys Ser Ser Gly  
 210 215 220

&lt;210&gt; 18

&lt;211&gt; 17

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (17)

<223> The C-terminal lysine is linked to an -NH<sub>2</sub> group

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Peptide

&lt;400&gt; 18

Cys Asp Gly Pro Lys Lys Lys Lys Lys Lys Ser Pro Ser Lys Ser Ser  
 1 5 10 15

Lys

&lt;210&gt; 19

&lt;211&gt; 15

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Peptide used  
 to generate SEQ ID NO.29

&lt;400&gt; 19

Ser Lys Asp Gly Lys Lys Lys Lys Lys Lys Ser Lys Thr Lys Cys  
 1 5 10 15

&lt;210&gt; 20

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Peptide used  
 to generate SEQ ID NO.30

&lt;400&gt; 20

Cys Ser Ala Ala Pro Ser Ser Gly Phe Arg Ile Leu Leu Leu Lys Val  
 1 5 10 15

&lt;210&gt; 21

&lt;211&gt; 17

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (1)

<223> The N-terminal glycine is linked to an  
 N-[Myristoyl]- group

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (17)

<223> The C-terminal cysteine is linked to  
 -S-S-[4-butyrimino]-N-epsilon(Lys) [Streptokinase]

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Conjugate of Streptokinase and MSWP-1

&lt;400&gt; 21

Gly Ser Ser Lys Ser Pro Ser Lys Lys Lys Lys Lys Lys Pro Gly Asp  
 1 5 10 15

Cys

&lt;210&gt; 22

&lt;211&gt; 527

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (478)

&lt;223&gt; Serine 478 is modified to:

O-4-CO-benzyl-NH(CH<sub>2</sub>)<sub>2</sub>NHCO(CH<sub>2</sub>)<sub>2</sub>-S-S-{Cys(-CONH<sub>2</sub>)-  
 Asp-Gly-Pro-Lys-Lys-Lys-Lys-Lys-Ser-Pro-Ser-Ly  
 s-Ser-Ser-Gly}-~NH-[Myristoyl]

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Reversible linkage of MSWP-1 to the active centre of Human Tissue-type Plasminogen Activator

&lt;400&gt; 22

Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met Ile Tyr Gln  
 1 5 10 15

Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn Arg Val Glu  
 20 25 30

Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser Val Pro Val  
 35 40 45

Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr Cys Gln Gln  
 50 55 60

Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu Gly Phe Ala  
 65 70 75 80

Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr Glu Asp Gln  
 85 90 95

Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser Gly Ala Glu  
 100 105 110

Cys Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro Tyr Ser Gly  
 115 120 125

Arg Asn Pro Asp Arg Asp Ser Lys Pro Trp Cys Tyr Val Phe Lys Ala  
 145 150 155 160  
 Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro Ala Cys Ser Glu Gly  
 165 170 175  
 Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr Arg Gly Thr His  
 180 185 190  
 Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn Ser Met Ile  
 195 200 205  
 Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala Gln Ala Leu  
 210 215 220  
 Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly Asp Ala Lys  
 225 230 235 240  
 Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr Trp Glu Tyr Cys  
 245 250 255  
 Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg Gln Tyr Ser Gln Pro  
 260 265 270  
 Gln Phe Arg Ile Lys Gly Gly Leu Phe Ala Asp Ile Ala Ser His Pro  
 275 280 285  
 Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser Pro Gly Glu Arg  
 290 295 300  
 Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile Leu Ser Ala  
 305 310 315 320  
 Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu Thr Val Ile  
 325 330 335  
 Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu Gln Lys Phe  
 340 345 350  
 Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe Asp Asp Asp Thr Tyr  
 355 360 365  
 Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp Ser Ser Arg Cys  
 370 375 380  
 Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu Pro Pro Ala Asp  
 385 390 395 400  
 Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser Gly Tyr Gly Lys  
 405 410 415  
 His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys Glu Ala His  
 420 425 430

Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr Arg Ser Gly  
450 455 460

Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp Ser Gly Gly  
465 470 475 480

Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu Val Gly Ile Ile  
485 490 495

Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val Pro Gly Val Tyr Thr  
500 505 510

Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg Asp Asn Met Arg Pro  
515 520 525

<210> 23

<211> 211

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: SCR1-3 with an  
additional 14 amino acid residues at the  
C-terminus

<400> 23

Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn  
1 5 10 15

Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu  
20 25 30

Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys  
35 40 45

Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys  
50 55 60

Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly  
65 70 75 80

Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg  
85 90 95

Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val  
100 105 110

Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu  
115 120 125

Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn  
130 135 140

Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly



Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr  
                   165                  170                  175

Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys  
                   180                  185                  190

Ile Ile Pro Asn Lys Asp Gly Pro Ser Glu Ile Leu Arg Gly Asp Phe  
                   195                  200                  205

Ser Ser Cys  
           210

<210> 24

<211> 228

<212> PRT

<213> Artificial Sequence

<220>

<221> UNSURE

<222> (211)..(212)

<223> Residues 1-211 are a first polypeptide chain and  
       residues 212-228 are a second polypeptide chain  
       linked by a disulphide bond formed between the  
       cysteines at positions 211 and 212

<220>

<221> UNSURE

<222> (228)

<223> The C-terminal glycine is linked to an  
       -NH-[Myristoyl] group

<220>

<223> Description of Artificial Sequence: SCR1-3 with an  
       additional C-terminal 14 amino acid residues  
       reacted with MSWP-1

<400> 24

Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn  
   1                  5                  10                  15

Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu  
           20                  25                  30

Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys  
           35                  40                  45

Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys  
       50                  55                  60

Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly  
       65                  70                  75                  80

Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg  
           85                  90                  95

Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu  
 115 120 125

Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn  
 130 135 140

Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly  
 145 150 155 160

Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr  
 165 170 175

Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys  
 180 185 190

Ile Ile Pro Asn Lys Asp Gly Pro Ser Glu Ile Leu Arg Gly Asp Phe  
 195 200 205

Ser Ser Cys Cys Asp Gly Pro Lys Lys Lys Lys Lys Lys Ser Pro Ser  
 210 215 220

Lys Ser Ser Gly  
 225

<210> 25

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide used with the oligonucleotide of  
 SEQ ID NO. 26 and plasmid pBC04-29 to generate  
 pBC04-31

<400> 25

cgcaccgcag tgcacatcc cgaacaaaga tggcccgagc gaaattctgc gtggcgattt 60  
 tagcagctgc ta 72

<210> 26

<211> 80

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide used with oligonucleotide of SEQ  
 ID NO. 25 and plasmid pBC04-29 to generate plasmid  
 pBC04-31

<400> 26

acgttagcag ctgctaaaat cgccacgcag aatttcgctc gggccatctt tgttcgggat 60  
 gatgcactgc ggtgcgggcc 80

<212> PRT  
 <213> Artificial Sequence

<220>  
 <221> UNSURE  
 <222> (1)  
 <223> The N-terminal glycine is linked to an  
 N-[Myristoyl]- group

<220>  
 <223> Description of Artificial Sequence:  
 Myristoyl/Electrostatic Swith Peptide Reagent 1  
 (MSWP-1)

<220>  
 <221> UNSURE  
 <222> (17)  
 <223> The cysteine at position 17 is (S-  
 2-Thiopyridyl)Cys-NH2

<400> 27  
 Gly Ser Ser Lys Ser Pro Ser Lys Lys Lys Lys Lys Lys Pro Gly Asp  
           1                  5                  10                  15

Cys

<210> 28  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <221> UNSURE  
 <222> (1)  
 <223> The N-terminal Cys is  
 N-acetyl-(S-2-thiopyridyl)Cys-

<220>  
 <221> UNSURE  
 <222> (17)  
 <223> The C-terminal lysine is  
 -(epsilonN-(Myristoyl))Lys-NH2

<220>  
 <223> Description of Artificial Sequence:  
 Myristoyl/Electrostatic Switch Peptide Reagent 2  
 (MSWP-2)

<400> 28  
 Cys Asp Gly Pro Lys Lys Lys Lys Lys Lys Ser Pro Ser Lys Ser Ser  
           1                  5                  10                  15

Lys

<210> 29  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <221> UNSURE  
 <222> (1)  
 <223> The N-terminal serine is N-(Myristoyl)-Ser-

<220>  
 <221> UNSURE  
 <222> (15)  
 <223> The C-terminal cysteine is  
 - (S-2-Thiopyrolyl)Cys-NH<sub>2</sub>

<220>  
 <223> Description of Artificial Sequence:  
 Myristoyl/Electrostatic Switch Peptide Reagent 3  
 (MSWP-3)

<400> 29  
 Ser Lys Asp Gly Lys Lys Lys Lys Lys Ser Lys Thr Lys Cys  
     1                    5                    10                    15

<210> 30  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <221> UNSURE  
 <222> (1)  
 <223> The N-terminal cysteine is  
 N-acetyl-(S-2-thiopyridyl)Cys-

<220>  
 <221> UNSURE  
 <222> (16)  
 <223> The C-terminal valine is -Val-NH(CH<sub>2</sub>)<sub>9</sub>CH<sub>3</sub>

<220>  
 <223> Description of Artificial Sequence: T-cell  
 targetting peptide reagent 1 (TCTP-1)

<400> 30  
 Cys Ser Ala Ala Pro Ser Ser Gly Phe Arg Ile Leu Leu Leu Lys Val  
     1                    5                    10                    15

<210> 31  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<222> (214)

<223> The C-terminal cysteine is  
-Cys-S-S-(CH<sub>2</sub>)<sub>2</sub>-CONH-(CH<sub>2</sub>)<sub>12</sub>CH<sub>3</sub>

<220>

<223> Description of Artificial Sequence: [SCR1-3/switch  
fusion]disulphide linked to [MAET]

<400> 31

Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn  
1 5 10 15

Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu  
20 25 30

Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys  
35 40 45

Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys  
50 55 60

Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly  
65 70 75 80

Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg  
85 90 95

Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val  
100 105 110

Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu  
115 120 125

Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn  
130 135 140

Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly  
145 150 155 160

Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr  
165 170 175

Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys  
180 185 190

Ile Ile Pro Asn Lys Asp Gly Pro Lys Lys Lys Lys Lys Lys Ser Pro  
195 200 205

Ser Lys Ser Ser Gly Cys  
210

<210> 32

<211> 17

<212> PRT

<213> Artificial Sequence

<221> UNSURE

<222> (1)

<223> The N-terminal Glycine is N-(Myristoyl)-Gly-

<220>

<221> UNSURE

<222> (17)

<223> The C-terminal cysteine is linked to an amino group and is also linked via a disulphide bond to -[4-butyrimino]-N-epsilon(Lys)[Rabbit anti-(human erythrocyte membrane) antibody].

<220>

<223> Description of Artificial Sequence: Rabbit anti-(human erythrocyte membrane) antibody-[MSWP-1] conjugate.

<400> 32

Gly Ser Ser Lys Ser Pro Ser Lys Lys Lys Lys Lys Lys Pro Gly Asp  
1 5 10 15

Cys

<210> 33

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: SCR1-3 with an additional C-terminal 18 amino acids

<400> 33

Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn  
1 5 10 15

Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu  
20 25 30

Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys  
35 40 45

Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys  
50 55 60

Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly  
65 70 75 80

Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg  
85 90 95

Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val  
100 105 110

Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn  
 130 135 140

Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly  
 145 150 155 160

Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr  
 165 170 175

Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys  
 180 185 190

Ile Ile Pro Asn Lys Ala Ala Pro Ser Val Ile Gly Phe Arg Ile Leu  
 195 200 205

Leu Leu Lys Val Gly Cys  
 210

<210> 34  
 <211> 84  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:  
 Oligonucleotide used with oligonucleotide of SEQ  
 ID NO.35 and plasmid pBC04-29 to generate plasmid  
 pBC04-34

<400> 34  
 cgcaccgcag tgcacatcc cgaacaaagc ggcgcccagc gtgattggct tccgtattct 60  
 gctgctgaaa gtggcgggct gcta 84

<210> 35  
 <211> 92  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:  
 Oligonucleotide used with the oligonucleotide of  
 SEQ ID NO. 34 and plasmid pBC04-29 to generate  
 plasmid pBC04-34

<400> 35  
 agcttagcag cccgccactt tcagcagcag aatacggag ccaatcacgc tgggcgccgc 60  
 ttgttcggg atgatgcact gcggtgcggg cc 92

<210> 36  
 <211> 231  
 <212> PRT  
 <213> Artificial Sequence

<223> Residues 1-214 are a first polypeptide chain and residues 215-231 are a second polypeptide chain linked by a disulphide bond formed between the cysteines at positions 214 and 215

<220>

<221> UNSURE

<222> (231)

<223> The C-terminal glycine is -Gly-NH-[Myristoyl]

<220>

<223> Description of Artificial Sequence: [SCR1-3] with an additional 18 C-terminal amino acid residues linked via a disulphide bond to MSWP-1

<400> 36

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Cys | Asn | Ala | Pro | Glu | Trp | Leu | Pro | Phe | Ala | Arg | Pro | Thr | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Thr | Asp | Glu | Phe | Glu | Phe | Pro | Ile | Gly | Thr | Tyr | Leu | Asn | Tyr | Glu |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Arg | Pro | Gly | Tyr | Ser | Gly | Arg | Pro | Phe | Ser | Ile | Ile | Cys | Leu | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Ser | Val | Trp | Thr | Gly | Ala | Lys | Asp | Arg | Cys | Arg | Arg | Lys | Ser | Cys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Asn | Pro | Pro | Asp | Pro | Val | Asn | Gly | Met | Val | His | Val | Ile | Lys | Gly |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Gln | Phe | Gly | Ser | Gln | Ile | Lys | Tyr | Ser | Cys | Thr | Lys | Gly | Tyr | Arg |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ile | Gly | Ser | Ser | Ser | Ala | Thr | Cys | Ile | Ile | Ser | Gly | Asp | Thr | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Trp | Asp | Asn | Glu | Thr | Pro | Ile | Cys | Asp | Arg | Ile | Pro | Cys | Gly | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Pro | Thr | Ile | Thr | Asn | Gly | Asp | Phe | Ile | Ser | Thr | Asn | Arg | Glu | Asn |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | His | Tyr | Gly | Ser | Val | Val | Thr | Tyr | Arg | Cys | Asn | Pro | Gly | Ser | Gly |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Arg | Lys | Val | Phe | Glu | Leu | Val | Gly | Glu | Pro | Ser | Ile | Tyr | Cys | Thr |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Asn | Asp | Asp | Gln | Val | Gly | Ile | Trp | Ser | Gly | Pro | Ala | Pro | Gln | Cys |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Ile | Pro | Asn | Lys | Ala | Ala | Pro | Ser | Val | Ile | Gly | Phe | Arg | Ile | Leu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |



Ser Pro Ser Lys Ser Ser Gly  
 225 230

<210> 37  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: illustrative amino acid sequence

<400> 37  
 Asp Gly Pro Lys Lys Lys Lys Lys Lys Ser Pro Ser Lys Ser Ser Gly  
 1 5 10 15

<210> 38  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: illustrative amino acid sequence

<400> 38  
 Gly Ser Ser Lys Ser Pro Ser Lys Lys Lys Lys Lys Lys Pro Gly Asp  
 1 5 10 15

<210> 39  
 <211> 20  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: illustrative amino acid sequence

<400> 39  
 Ser Pro Ser Asn Glu Thr Pro Lys Lys Lys Lys Lys Arg Phe Ser Phe  
 1 5 10 15

Lys Lys Ser Gly  
 20

<210> 40  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>

&lt;400&gt; 40

Asp Gly Pro Lys Lys Lys Lys Lys Lys Ser Pro Ser Lys Ser Ser Lys  
 1 5 10 15

&lt;210&gt; 41

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: illustrative amino acid sequence

&lt;400&gt; 41

Ser Lys Asp Gly Lys Lys Lys Lys Lys Ser Lys Thr Lys  
 1 5 10

&lt;210&gt; 42

&lt;211&gt; 6

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: illustrative amino acid sequence

&lt;400&gt; 42

Gly Arg Gly Asp Ser Pro  
 1 5

&lt;210&gt; 43

&lt;211&gt; 13

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: illustrative amino acid sequence

&lt;400&gt; 43

Asp Gly Pro Ser Glu Ile Leu Arg Gly Asp Phe Ser Ser  
 1 5 10

&lt;210&gt; 44

&lt;211&gt; 17

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: illustrative amino

&lt;400&gt; 44

Gly Asn Glu Gln Ser Phe Arg Val Asp Leu Arg Thr Leu Leu Arg Tyr  
 1 5 10 15

Ala

&lt;210&gt; 45

&lt;211&gt; 9

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: illustrative amino  
 acid sequence

&lt;400&gt; 45

Gly Phe Arg Ile Leu Leu Leu Lys Val  
 1 5

&lt;210&gt; 46

&lt;211&gt; 15

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: illustrative amino  
 acid sequence

&lt;400&gt; 46

Ser Ala Ala Pro Ser Ser Gly Phe Arg Ile Leu Leu Leu Lys Val  
 1 5 10 15

&lt;210&gt; 47

&lt;211&gt; 17

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: illustrative amino  
 acid sequence

&lt;400&gt; 47

Ala Ala Pro Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala  
 1 5 10 15

Gly

&lt;210&gt; 48

&lt;211&gt; 17

&lt;212&gt; PRT

<220>

<223> Description of Artificial Sequence: illustrative amino acid sequence

<400> 48

Asp Gly Pro Lys Lys Lys Lys Lys Lys Ser Pro Ser Lys Ser Ser Gly  
1 5 10 15

Cys

<210> 49

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: illustrative amino acid sequence

<400> 49

Ala Ala Pro Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala  
1 5 10 15

Gly Cys

<210> 50

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: illustrative amino acid sequence

<400> 50

Asp Gly Pro Ser Glu Ile Leu Arg Gly Asp Phe Ser Ser Cys  
1 5 10

<210> 51

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: illustrative DNA oligonucleotide

<400> 51

cctctggcca aatgtacctc tcgtgcacat tgctga